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FOOT* E09/5860

5' GTCGAGGATCCCTAAAGTCCTTTGAA'GCTTTCCCTTACA -900
 GTGAGATGGGATCCAGTATTTATTGAGTTTCCCTCATTCATAAAATGGGGATAATAATAGTAAATGAGTGTCTC -825
 GCGCTAAGACAGTGGAAATAGTGGCTGGCCACAGATAAGCCCTCGGTAAATGGTAGCCAATAATGATAGAGTGTCTG -750
 TAAGATAGTCTTTTCTCTCCTCTCTCTCAACAAGTCTCTTAATCAATTTATTCACCTTTTATAACAGGAATAGAACTA -675
 AGACATTAGCACTTTCCAAAGGTCGCTAGCAAGTAATGGAGAGACCCCTATGACCAGGATGAAAGCAAGAAATTTCCC -600
 ATAAGAGGACTCATTTCCAACTCATATCTTTGTGAAAAGGTTCCCAATGCCCCAGCTCAGATCAACTGCCTCAATTTA -525
 CAGTGTGAGTGTCTACCTCCTTTGGGACTGTATATCCAGAGGACCCCTCCTCAATAAAACACTTTTATAAATAA -450
 CATCCTTCCATGGATGAGGAAAGGAGGTAAGATCTGTAAATGAATAAGCAGGAACCTTTGAAGACTCAGTGACTCA -375
 GTGATAATAAGACTCAGTACTTCTGTATCTCTGTCTTAACTGCTCCCAACTCCTTTGGTTGTCCCCAAGAAAGCGGT -300
 TCCTGCTCTCTCTGAGAGGACCCCTCCCTGGAAAGGTAAACTAAGGATGTCAGCAGAGAAATTTTCCACCATTG -225
 GTGCTTGGTCAAGAGGAAACTGATGAGCTCGACTCTAGATGTGTGTGTCAGTGAGCGAGAGACAGAGACTCGAAT -150
 TTCCGGAGGCTATTTTCAGTTTCTTTTCCGTTTGTGCAATTTTCACTTATGATACCGGCCAATGCTTGGTTGCT -75
 ATTTTGGAAACTCCCTTAGGGATGCCCCCTCACTGCCCCATPAAAGGGCCGCTGAGCTGCAGAGGATTCCTGC 1
 AGAGATCAAGACAGCAGCTGGACCTCGCACAGCCCTCTCCCCACAGGTACCATG +75
 NFE-2
 ets-1
 AP-1/
 myb
 TCF-1
 GATA
 TCF-1
 CD28 Res. El.
 NF-
 NFIL-6
 CCAAT box
 NFkB
 MyoD
 TATAA box
 translational start

FIG. 1

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AGAAGGCCTTACAGTGAGATGGGATCCCAGTATTTATTGAGTTTCCTCATT CATAAAAATG -848
RA1 →

GGGATAATAATAGTAAATGAGTTGACACGCGCTAAGACAGTGGAATAGTGGCTGGCACAG -788
ATAAGCCCTCGGTAAATGGTAGCCAATAATGATAGAGTATGCTGTAAGATATCTTTCTCT -728
CCCTCTGCTTCTCAACAAGTCTCTAATCAATTATCCACTTTATAAACAAGGAAATAGAA -668
CTCAAAGACATTAAGCACTTTTCCCAAAGGTCGCTTAGCAAGTAAATGGGAGAGACCCTA -608

*

TGACCAGGATGAAAGCAAGAAATTCCCACAAGAGGACTCATTCCAACCTCATATCTTGTGA -548
AAAGGTTCCCAATGCCAGCTCAGATCAACTGCCTCAATTTACAGTGTGAGTGTGCTCAC -488
CTCCTTTGGGGACTGTATATCCAGAGGACCCTCCTCAATAAAACACTTTATAAATAACAT -428

RA2F →

CCTTCCATGGATGAGGGAAAGGAGGTAAGATCTGTAATGAATAAGCAGGAACCTTTGAAGA -368
-403

CTCAGTGACTCAGTGAGTAATAAAGACTCAGTGACTTCTGATCCTGTCCTAACTGCCACT -308
← RA2R

CCTTGTTGTCCCCAAGAAAGCGGCTTCCTGCTCTCTGAGGAGGACCCCTTCCCTGGAAGG -248

*

TAAAACTAAGGATGTCAGCAGAGAGAAATTTTCCACCATTGGTGCTTGGTCAAAGAGGAAA -188
CTGATGAGCTGACTCTAGATGAGAGAGCAGTGAGGGAGAGACAGAGACTCGAATTTCCGG -128

SacI

AGGCTATTT CAGTTTT CTTTT CCGTTTT GTGCAATTT CACTTAT GATACCGG CCAATGCT -68
* NF IL-6 CCAAT

TGGTTGCTATTTTGGAAACTCCCCTTAGGGGATGCCCCTCAACTGGCCCTATAAAGGGCC -8
NFkB NFkB -28 TATA

▼ Start of transcription

AGCCTGAGCTGCAGAGGATTCTGCAGAGGATCAAGACAGCACGTGGACCTCGCACAGCC 53
1 *****

TCTCCACAGGTACCATGAAGGTCTCCGCGGACGCCCTCGCTGTCATCCTCATTGCTACT 113
KpnI ← RA3

GCCCTCTGCGC 124

FIG. 2

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CLUSTAL W (1.8) multiple sequence alignment

```
new      old      6
GTCGAGGATCCCTAAAGTCCTTTGAAGCCTTCATATCTGTAACTTTTGTGCCAAGAAGG 60
-----AGAAAGG
*****

new      old      66
CCTTACAGTGAGATGGGATCCAGTATTTATTGAGTTTCCTCATTCATAAAATGGGGATA 66
CCTTACAGTGAGATGGGATCCAGTATTTATTGAGTTTCCTCATTCATAAAATGGGGATA 120
*****

new      old      126
ATAATAGTAAATGAGTTGACACGGCGCTAAGACAGTGGAATAGTGGCTGGCACAGATAAGC 126
ATAATAGTAAATGAGTTGACACGGCGCTAAGACAGTGGAATAGTGGCTGGCACAGATAAGC 180
*****

new      old      186
CCTCGGTAATGGTAGCCCAATATGATAGAGTATGCTGTAAGATATCTTTCTCTCCCTCT 186
CCTCGGTAATGGTAGCCCAATATGATAGAGTATGCTGTAAGATATCTTTCTCTCCCTCT 240
*****

new      old      246
GCTTCTCAACAAGTCTCTAATCAATTATTCACCTTTATAAACAAGGAATAGAACTCAA 246
GCTTCTCAACAAGTCTCTAATCAATTATTCACCTTTATAAACAAGGAATAGAACTCAA 300
*****

new      old      306
GACATTAAAGCACCTTTTCCAAAGGTCGCTTAGCAAGTAAATGGGAGAGACCCCTATGACCA 306
GACATTAAAGCACCTTTTCC-AAAGGTCGCTTAGCAAGTAAATGGGAGAGACCCCTATGACCA 359
*****
```

FIG. 3(a)

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TOTAL 597560

new	GGATGAAGCAAGAAATTCACCAAGAGGACTCATTCCAACATCATATCTTGTAAGGTT	366
old	GGATGAAGCAAGAAATTCACCAAGAGGACTCATTCCAACATCATATCTTGTAAGGTT	419

new	TCCCAATGCCCAGCTCAGATCAACTGCTCAATTTACAGTGTGAGTGTGCTCACCTCCTT	426
old	TCCCAATGCCCAGCTCAGATCAACTGCTCAATTTACAGTGTGAGTGTGCTCACCTCCTT	479

new	TGGGACTGTATATCCAGAGGAGCCCTCCTCAATAAAACACTTTATAAATAACATCCTTCC	486
old	TGGGACTGTATATCCAGAGGAGCCCTCCTCAATAAAACACTTTATAAATAACATCCTTCC	539

new	ATGGATGAGGGAAGGAGATAAGATCTGTAATGAATAAGCAGGAACCTTTGAAGACTCAGT	546
old	ATGGATGAGGGAAGGAGATAAGATCTGTAATGAATAAGCAGGAACCTTTGAAGACTCAGT	599

new	GACTCAGTGAGTATAAAGACTCAGTGACTTCTGATCCTGTCTTAAGTCCCTTGT	606
old	GACTCAGTGAGTATAAAGACTCAGTGACTTCTGATCCTGTCTTAAGTCCCTTGT	659

new	TGTCCCCAAGAAAGCGGCTTCCTGCTCTCTGAGGAGGACCCCTTCCCTGGAAGGTAAAC	666
old	TGTCCC-AAGAAAGCGGCTTCCTGCTCTCTGAGGAGGACCCCTTCCCTGGAAGGTAAAC	718

new	TAAGGATGTCAGCAGAGAGAAATTTTCCACCATTTGGTCAAGAGGAACTGATG	726
old	TAAGGATGTCAGCAGAGAGAAATTTTCCACCATTTGGTCAAGAGGAACTGATG	778

FIG. 3(b) (cont'd)

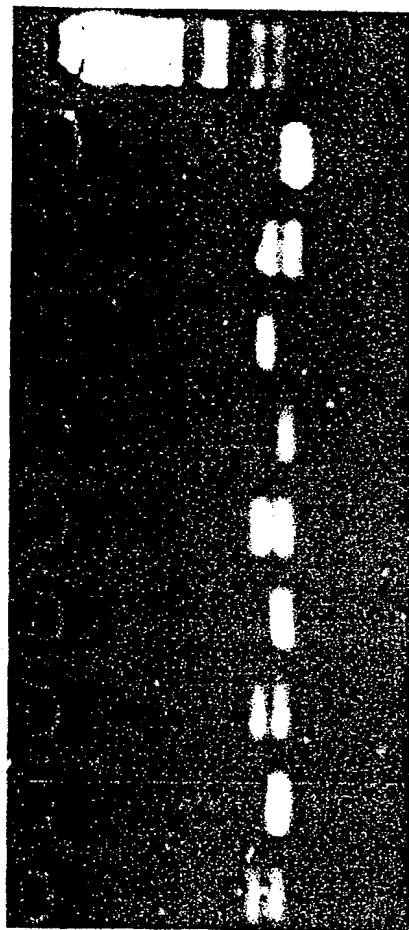
[illegible]

FIG. 3(c) (cont'd)

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RANTES gene promoter polymorphism RFLP analysis

1 2 3 4 5 6 7 8 9



Mutant

135 bp

Wild type

112bp

Lanes 2, 4, 6, & are homozygote wild types

Lane 7 is homozygote mutant

Lanes 1, 3, 5 & 8 are heterozygotes

FIG. 4

Results

Group	GG	GA	AA	G	A
non-atopic/non-asthmatic	14 (0.61)	9 (0.39)	0 (0.00)	37 (0.80)	9 (0.20)
Atopic/non-asthmatic	37 (0.53)	30 (0.43)	3 (0.04)	104 (0.74)	36 (0.26)
Asthmatic/non-atopic	3 (0.43)	3 (0.43)	1 (0.14)	9 (0.64)	5 (0.36)
Atopic and asthmatic	19 (0.48)	16 (0.40)	5 (0.12)	54 (0.68)	26 (0.32)
Haemophiliacs HIV +	63 (0.69)	22 (0.24)	6 (0.07)	148 (0.81)	34 (.19)
Haemophiliacs HIV -	9 (0.69)	4 (0.31)	0 (0)	22 (0.85)	4 (0.15)
HIV exposed-uninfected	10 (0.48)	7 (0.33)	4 (0.19)*	31 (0.74)	11 (0.26)
Controls	66 (0.73)	19 (0.21)	5 (0.06)	151 (0.84)	29 (0.16)

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* encoding AA or AG in exposed un-infected carries an OR of 3.0 (1.0 9 0) p 0.022 over encoding GG genotype, when compared with the controls.

FIG. 5

FOOT* E09/5B60

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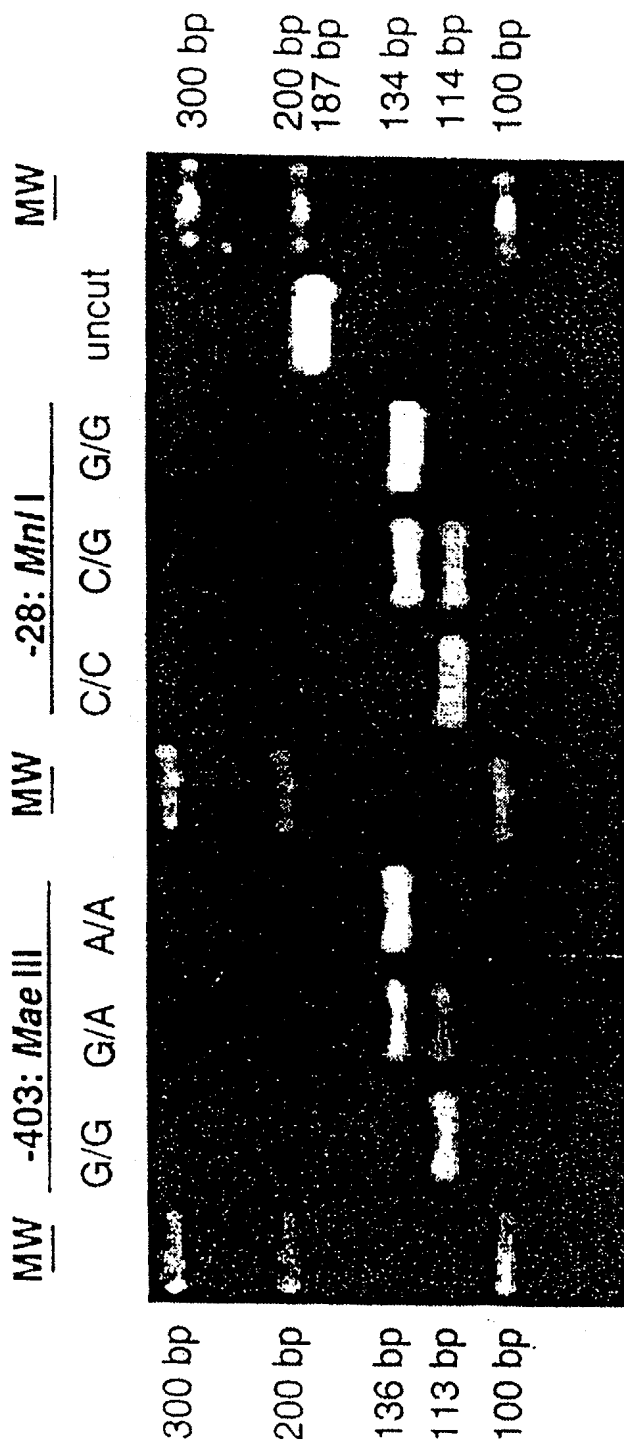


FIG. 6

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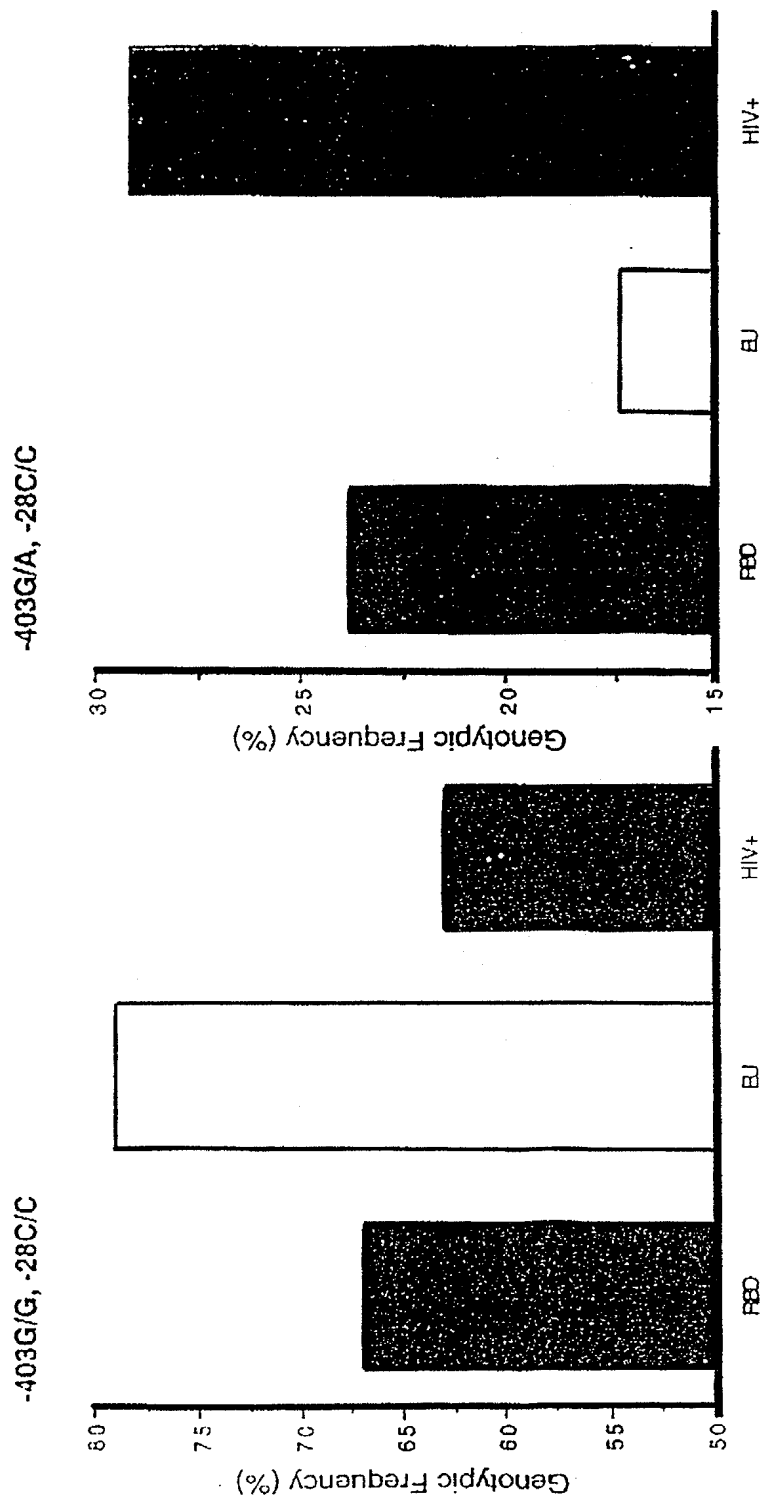


FIG. 7

FOOTNOTES

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Proportion Free of AIDS after Seroconversion by RANTES Genotype

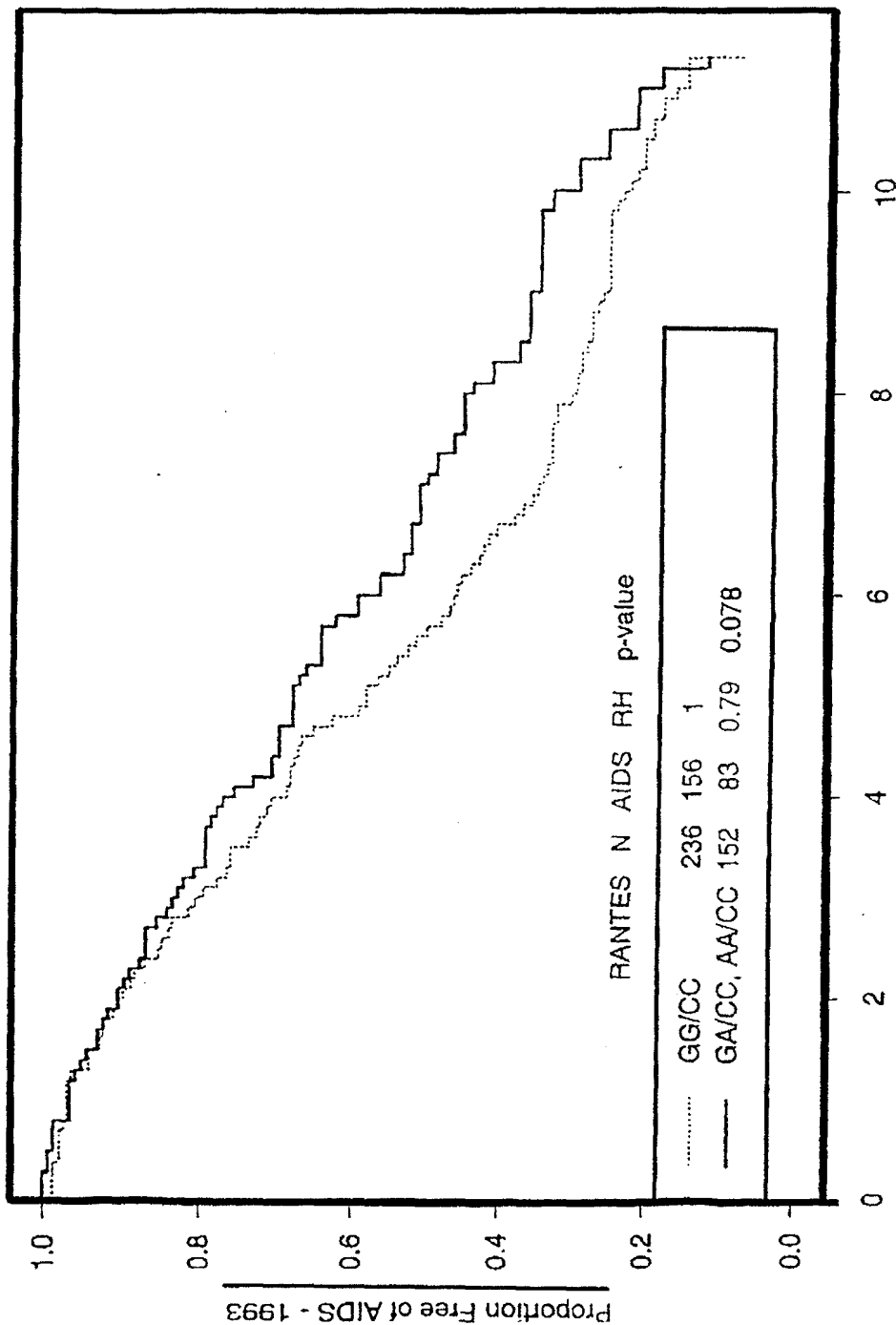


FIG. 8

Time from Seroconversion (Years)